

File
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BIOTECHNOLOGY
SYSTEMS
BRANCH



#8

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/208,629

Source: 1646

Date Processed by STIC: 7/10/2000

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1646

RAW SEQUENCE LISTING DATE: 07/10/2000
 PATENT APPLICATION: US/09/208,629 TIME: 12:18:59

Input Set : A:\22000-20603.10-Seq.txt
 Output Set: N:\CRF3\07102000\I208629.raw

SEQUENCE LISTING

C--> 5 (1) GENERAL INFORMATION:
 7 (i) APPLICANT: Coughlin, Shaun
 8 Ishihari, Hiroaki
 9 Connolly, Andrew
 C--> 11 (ii) TITLE OF INVENTION: Protease Activated Receptor
 12 3 and Uses Thereof
 14 (iii) NUMBER OF SEQUENCES: 23
 16 (iv) CORRESPONDENCE ADDRESS:
 17 (A) ADDRESSEE: MORRISON & FOERSTER
 18 (B) STREET: 755 Page Mill Road
 19 (C) CITY: Palo Alto
 20 (D) STATE: California
 21 (E) COUNTRY: USA
 22 (F) ZIP: 94304-1018
 24 (v) COMPUTER READABLE FORM:
 25 (A) MEDIUM TYPE: Diskette
 26 (B) COMPUTER: IBM Compatible
 27 (C) OPERATING SYSTEM: DOS
 28 (D) SOFTWARE: FastSEQ for Windows Version 2.0
 C--> 30 (vi) CURRENT APPLICATION DATA:
 31 (A) APPLICATION NUMBER: US/09/208,629
 C--> 32 (B) FILING DATE: 22-Jun-2000
 33 (C) CLASSIFICATION:
 35 (vii) PRIOR APPLICATION DATA:
 36 (A) APPLICATION NUMBER: 08/742,440
 37 (B) FILING DATE: 30-OCT-1996
 39 (viii) ATTORNEY/AGENT INFORMATION:
 40 (A) NAME: Catherine M. Polizzi
 41 (B) REGISTRATION NUMBER: 40,130
 42 (C) REFERENCE/DOCKET NUMBER: 22000-20604.00
 44 (ix) TELECOMMUNICATION INFORMATION:
 45 (A) TELEPHONE: (650) 813-5600
 46 (B) TELEFAX: (650) 494-0792
 47 (C) TELEX: 706141

Does Not Comply
 Corrected Diskette Needed

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ERRORED SEQUENCES

464 (2) INFORMATION FOR SEQ ID NO: 10:
 466 (i) SEQUENCE CHARACTERISTICS:
 467 (A) LENGTH: 29 base pairs
 468 (B) TYPE: nucleic acid
 469 (C) STRANDEDNESS: double
 470 (D) TOPOLOGY: linear
 472 (ii) MOLECULE TYPE: cDNA
 473 (ix) FEATURE:

RAW SEQUENCE LISTING DATE: 07/10/2000
 PATENT APPLICATION: US/09/208,629 TIME: 12:18:59

Input Set : A:\22000-20603.10-Seq.txt
 Output Set: N:\CRF3\07102000\I208629.raw

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481      (A) NAME/KEY: Other
476      (B) LOCATION: 1...29
477      (D) OTHER INFORMATION: N=Inosine at residues 3, 12, 18, 21, and 24
486      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
E--> 488 GTNTACATGC TNMACYTNGC NNTNGCNGA
490 (2) INFORMATION FOR SEQ ID NO: 11:
492      (i) SEQUENCE CHARACTERISTICS:
493          (A) LENGTH: 26 base pairs
494          (B) TYPE: nucleic acid
495          (C) STRANDEDNESS: double
496          (D) TOPOLOGY: linear
498      (ii) MOLECULE TYPE: cDNA
499      (ix) FEATURE:
500          (A) NAME/KEY: Other
501          (B) LOCATION: 6...21
502          (D) OTHER INFORMATION: N=Inosine at residue 6, 9, 12, 15, and 21
504      (ix) FEATURE:
505          (A) NAME/KEY: Other
506          (B) LOCATION: 24
507          (D) OTHER INFORMATION: N=A or C or G or T at residue 24
509      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
E--> 511 GGATANACNA CMGCNADRWA NCKBIC
687 (2) INFORMATION FOR SEQ ID NO: 23:
689      (i) SEQUENCE CHARACTERISTICS:
690          (A) LENGTH: 9 amino acids
691          (B) TYPE: amino acid
692          (C) STRANDEDNESS: single
693          (D) TOPOLOGY: linear
696      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
698 Thr Phe Arg Gly Ala Pro Pro Asn Ser
699 1 5
E--> 700 1
E--> 703 1

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*29 ← insert cumulative base
 total at end of each
 line*

B is at location 24

26 ← insert

delete at end of file

VERIFICATION SUMMARY DATE: 07/10/2000
PATENT APPLICATION: US/09/208,629 TIME: 12:19:00

Input Set : A:\22000-20603.10-Seq.txt
Output Set: N:\CRF3\07102000\I208629.raw

L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:11 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:30 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]
L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:94 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=2, Value=[]
L:128 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:128 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=3, Value=[Xaa = stop]
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:262 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:262 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=6, Value=[Xaa = stop]
L:266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:488 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:488 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:488 M:204 E: No. of Bases differ, LENGTH:Input:29 Counted:0 SEQ:10
L:511 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:511 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:511 M:204 E: No. of Bases differ, LENGTH:Input:26 Counted:0 SEQ:11
L:648 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=20, Value=[]
L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:665 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=21, Value=[]
L:667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:700 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
M:332 Repeated in SeqNo=23

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